

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 22:15:02 ; Search time 5994 Seconds

(without alignments)
4808.662 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 665 1 MAHEMIGTQYTERLVALL.....LKVSGSSFSGSMIEIVS 665

Scoring table: OLIGO

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 473

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:

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41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	665	100.0	5450	6 AX482439	AX482439 Sequence
2	665	100.0	5450	6 AX482478	AX482478 Sequence

ALIGNMENTS

RESULT 1
AX482439
LOCUS AX482439 5450 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 108 from Patent WO02057460.
ACCESSION AX482439
VERSION AX482439.1 GI:22316984
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
Toddard,C.G., Bol,D., Pinger,J., Lee,L., Nelson,T., Schieven,G., Suchard,S., Banae,D., Basolino,D., Feder,J., Kyteck,S., Wcatree,P., Mintier,G., Siemera,N., Jackson,D.G. and Ramamathan,C. Polynucleotides encoding human phosphatases
Patent: WO 02057460-A 108 25-JUL-2002;
JOURNAL SQUIBB BRISTOL MYERS CO (US)
FEATURES
source location/Qualifiers
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ORIGIN

Alignment Scores:

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 21 SerGlyThrgIuLysValLeuLeuLeuAAspSerArgProPheValGluTyraThrSer 40
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QY 121 LeuAlaGlyValPheAlaGluPheSerArgCysePheProGlyLeuCyseGluGlyLysSer 140
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QY 161 ArgIleLeuProAsnLeuTyrlLeuGlyCyseGlnArgAspValLeuAsnLysGluLeuIle 180
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QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
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QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrlThrSerPheLeuPheGly 520
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QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerSerAlaGlyLeuGlyLysGlyTyrlHis 540
Db 2098 CTTTCACACAGCAGACACACACTCAGAAATCTGTGCTGGCTTAAGGCTGGCAGC 2157
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrlTyrlPheAla 560
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QY 601 GlnLysProSerAspAlaArgAlaAspSerArgArgSerTyrlHisGluGluSerProPheGlu 620
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RESULT 2

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DEFINITION	AX482478				
ACCESSION	AX482478.1	GI:22316999			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1				
TITLE	Todderd,C.G., Bol,D., Finger,J., Lee,L., Nelson,T., Schieven,G., Suchard,S., Banae,D., Bassolino,D., Feder,J., Krysek,S., Mcatee,P., Minter,G., Siemers,N., Jackson,D.G. and Kamanathan,C. Polynucleotides encoding human phosphatases				
JOURNAL	Patent: WO 02057460-A 147 25-JUL-2002;				
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QY	41	HISileleuGluAlaleuAsnileAenCYserLYSleuMetLYArgArgleuGlnGln	60		
DB	658	CACATTTTGGAGCAATTATATCAACTGCTCCAGCTTATACAGCAAGAGTTGCAACG	717		
QY	61	AapLYSValleuileThrgluLeuileGlnHISerAlaLYSHISLYValAlaSPllleAap	80		
DB	718	GACAAAGCTTAAATACAGAGCTCATCCGCAITTCAGCGAAACATTAAGTTACATTGAT	777		
QY	81	CYSserGlnLYSValValValTYraPrgInSerSergInaSPValAlaSerLeuSerSer	100		
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QY	341	CYSAlaAapSerAlaThrSergluAlaAlaGlyGlnArgProValHISProAlaSerVal	360		
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QY	361	ProSerValProSerValGlnProSerleuLeuGluAapSerProleuValGlnAlaLeu	380		
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QY	441	LYSleuCYSGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro	460		
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QY 501 SerProLeuHisArgSerGlySerValGlnAspAsnTyrHisThrSerPheLeuPheGly 520
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QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrPheHis 540
Db 2098 CTTTCCACAGCCAGCAGCAGCAGCTCAGCAAGTCTGCTGGCCTTAAGGGCTGGCAC 2157
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
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Db 2518 ATCATTGAGGTCTCC 2532

Search completed: June 24, 2004, 01:46:29
Job time : 6003 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 19:31:01 ; Search time 615 Seconds
(without alignments)
4593.580 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 665
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Scoring table:
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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 473

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:

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-USER=US10029345 @CGML 1.1 708 @runat.23062004.121751.25585 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUTERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N Geneseg 29Jan04:*

- 1: geneseg1980s:*
- 2: geneseg1990s:*
- 3: geneseg2000s:*
- 4: geneseg2001as:*
- 5: geneseg2001bs:*
- 6: geneseg2002as:*
- 7: geneseg2003as:*
- 8: geneseg2003bs:*
- 9: geneseg2003cs:*
- 10: geneseg2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	665	100.0	5450	6	ACCG0559 Polynucle
2	665	100.0	5450	6	ACCG0572 Polynucle

ALIGNMENTS

RESULT 1
ACCG0559

ID	ACCG0559	strand:	cdna; 5450 BP.
XX	ACCG0559;		
AC	ACCG0559;		
XX	19-JUN-2003	(first entry)	
DT	19-JUN-2003	(first entry)	
XX	Polynucleotide relating to the invention SEQ ID NO: 108.		
DE	Gene; ss; antiproliferative; hepatotropic; nephrotoxic; antiarthritic;		
XX	antiproliferative; cardiact; cyostatic; gene therapy; liver disease;		
KW	proliferative disorder; renal failure; cardiovascular disorder;		
KM	immunological disorder; arthritis; psoriasis; congenital heart defect;		
KW	congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	MO200257460-A2.		
PN	MO200257460-A2.		
XX	25-UTL-2002.		
PD	25-UTL-2002.		
XX	20-DEC-2001; 2001WO-US050459.		
PF	20-DEC-2001; 2001WO-US050459.		
XX	20-DEC-2000; 2000US-0256868P.		
PR	30-MAR-2001; 2001US-0280186P.		
PR	01-MAY-2001; 2001US-0287735P.		
PR	05-JUN-2001; 2001US-0295848P.		
PR	25-JUN-2001; 2001US-0300465P.		
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.		
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.		
XX	Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;		
PI	Stiemers N, Boi D, Schieven G, Finger J, Todderud CG, Bassolino D;		
PI	Krystek S, Mcatee P, Suchard S, Banas D;		
XX	WPI; 2002-599721/64.		
DR	P-PDSB; ABR52381.		
XX	Novel polynucleotides encoding human phosphatase polypeptides useful in		
PT	the prevention or treatment of e.g. proliferative and cardiovascular		
PT	disorders.		
XX	Claim 1; Fig 13; 801pp; English.		
PS	Claim 1; Fig 13; 801pp; English.		
XX	The invention relates to a novel isolated nucleic acid comprising a		
CC	polynucleotide having a nucleotide sequence selected from 40		
CC	polynucleotides fully defined in the specification. The polynucleotide of		
CC	the invention has antiproliferative, hepatotropic, nephrotoxic,		
CC	antiarthritic, antiproliferative, cardiact, and cyostatic activity. The		
CC	polynucleotide may have a use in gene therapy. A polynucleotide or		
CC	polypeptide of the invention is useful for preventing, treating or		
CC	ameliorating a medical condition, e.g. a proliferative disorder. They are		
CC	also useful for treating e.g. liver disease, renal failure, immunological		
CC	disorders including arthritis and psoriasis, cardiovascular disorders		
CC	such as congenital heart defects and congestive heart failure, and		
CC	cancer. A method of the invention is useful for diagnosing a pathological		
CC	condition or susceptibility to a condition in a subject. The present		
CC	sequence is used in the exemplification of the invention		
XX	Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;		
SQ	Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;		
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Score:	665.00	Matches:	665
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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Db	538 ATGGCCCATGAGATGATTGGAACTCAATTGTTACTGAGAGGTGGCTGCTGCGAA 597		

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QY 21 SerGIYThrGIuLysValLeuLeuIleAspSerArgProPheValGIuTYrAsnThrSer 40
Db 598 AGTGAAGCGAAGAAAGTCTGCTGTAATGATAGCCGGCATTTGGGAATACAAATACATCC 657
QY 41 HisIleuGIuAlaIleAsnIleAspCysSerIysLeuMetLysArgArgLeuGIuGln 60
Db 658 CACATTTTGGAAAGCCATTAAATACACTGCTCCAGCTTATGAAAGCGAAGGTGCACAG 717
QY 61 AspLysValLeuIleThrGIuLeuIleGlnHisSerAlaLysSHISLysValAspIleAsp 80
Db 718 GACAAAGGTAAATACAGAGCTCATCCAGCATTCAGGAAACAAATAGATTGACATTGAT 777
QY 81 CysSerGIuLysValValValTYrAspGlnSerSerGIuAspValAlaSerLeuSerSer 100
Db 778 TGCAGTCGAAGAGTTGATGTTACGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 837
QY 101 AspCysPheLeuThrValLeuLeuGIYLSLeuGIuLysSerPheAsnSerValHisLeu 120
Db 838 GACTGTTTCTCACGTACTCTGGGTAACTGGAGAAAGACTTCMACTCTGTTCACTG 897
QY 121 LeuAlaGIYGIYpheaIaGIuPheSerArgCysPheProGIYLeuCysGIuGIYLysSer 140
Db 898 CTTCCAGGTGGGTGGTGGAGTCTCTGTTGTTCCCTGGCTCTGTGAAGCAAAATCC 957
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGIYProThr 160
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QY 241 LeuValHisCysLeuAlaGIYIleSerArgSerAlaThrIleAlaIleAlaTYrIleMet 260
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QY 401 SerLeuAspIleLysSerValSerTYrSerAlaSerMetAlaIaSerLeuHisGIYpHe 420
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QY 561 ThrGlnSerSerHisPheTYrSerAlaSerAlaIleTYrGIYGIYSerAlaSerTYrSer 580
Db 2218 ACGAGTCTTCACTTACTTCTGCTCAGCACTTACGAGGAGGCGAGTGCAGTTACTCT 2277
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Db 2278 GCTACAGCTGCAGCAGCTGCCCACTTGGCAGACCAAGTCTATCTGTGCGAGGCGG 2337
QY 601 GlnLysProSerSerAspArgAlaAspSerArgArgSerTPHisGIuLysProPheGln 620
Db 2338 CAGAAAGCCAAAGACAGAGCTGACTCGCGGCGAGCTGGCATGAAAGAGGCCCTTTGAA 2397
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RESULT 2
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ID ACC60572 standard; cDNA, 5450 BP.
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AC AC60572;
XX
XX 19-JUN-2003 (first entry)
XX
DE Polynucleotide relating to the invention SEQ ID NO: 147.
XX
KW Gene; ss; antiproliferative; hepatotropic; nephrotropic; antiarthritic;
KW antiproliferative; cardiant; cytostatic; gene therapy; liver disease;
KW proliferative disorder; renal failure; cardiovascular disorder;
```

KW immunological disorder; arthritis; psoriasis; congenital heart defect;
 KW congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
 OS Homo sapiens.
 XX MO200257460-A2.
 PN 25-JUL-2002.
 PD 25-JUL-2002.
 PF 20-DEC-2001; 2001MO-US050459.
 XX 20-DEC-2001; 2001US-0256686P.
 PR 20-MAR-2000; 2000US-0256686P.
 PR 30-MAR-2001; 2001US-0280186P.
 PR 01-MAY-2001; 2001US-0287735P.
 PR 05-JUN-2001; 2001US-0295848P.
 PR 25-JUN-2001; 2001US-0300465P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA Jackson DG, Feder J, Nelson T, Mintler G, Ramanathan C, Lee L,
 PI Slemers N, Bol D, Schlieven G, Finger J, Todderud CG, Bassolino D,
 PI Kyarek S, Mcatee P, Suchard S, Banas D;
 XX MPI; 2002-599721/64.
 DR P-PSDB; ABR52407.
 XX Novel polynucleotides encoding human phosphatase polypeptides useful in
 PT the prevention or treatment of e.g. proliferative and cardiovascular
 PT disorders.
 XX Example 7; Fig 19; 801pp; English.
 XX The invention relates to a novel isolated nucleic acid comprising a
 CC polynucleotide having a nucleotide sequence selected from 40
 CC polynucleotides fully defined in the specification. The polynucleotide of
 CC the invention has antiproliferative, hepatotropic, nephrotropic, the
 CC anticholelithic, antipsoriatic, cardiant, and cytostatic activity. The
 CC polynucleotide may have a use in gene therapy. A polynucleotide or
 CC polypeptide of the invention is useful for preventing, treating or
 CC ameliorating a medical condition, e.g. a proliferative disorder. They are
 CC also useful for treating e.g. liver disease, renal failure, immunological
 CC disorders including arthritis and psoriasis, cardiovascular disorders
 CC such as congenital heart defects and congestive heart failure, and
 CC cancer. A method of the invention is useful for diagnosing a pathological
 CC condition or susceptibility to a condition in a subject. The present
 CC sequence is used in the exemplification of the invention
 XX
 SQ Sequence 5450 BP; 1471 A; 1211 C; 1337 G; 1431 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 5450
 Score: 665.00 Matches: 665
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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 QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
 DB 598 AGTGGAAAGGAAAAGTCTGCTAATTGATGACCGGCATTGTGGAAATCAATACATCC 657
 QY 41 HisIleLeuGluValIleAsnIleAsnGlySerIleLeuMetIleAsnArgLeuGlnGln 60
 DB 658 CACATTTGGAAACCATTAATATCACTGCCAAGCTTATGAAGCAAGGTTGCAACAG 717
 QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerIleValIleValIleAsp 80

DB 718 GACAAAGTGTATTAATACAGACTCATCCAGCATTCAGCAAAACATAGGTGACATTGAT 777
 QY 81 CysSerGlnIleValValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
 DB 778 TGCAGTCAGAAAGTGTAGTTAATGATCAAGCTCCCAAGATGTTCCCTCTCTCTTCA 837
 QY 101 AspCysPheLeuThrValLeuLeuGluIleValSerPheAsnSerValHisLeu 120
 DB 838 GACTGTTTCTCAGTACTCTTGGGTAAACTGGAGAAAGCTTCAACTGTTCACCTG 897
 QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyIleSer 140
 DB 898 CTTCGAGTGGGTTCAGTTCAGTTCCTCTGTTTCCCTGCTGTGAGGAAATCC 957
 QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
 DB 958 ACTCATGCTCCATACCTGCAATTCCTCAGCTTGCTTACTGTCGCAACATTTGGCCCAACC 1017
 QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnIleGlyLeu 180
 DB 1018 CGAATCTTCCCAATCTTATCTTGCTGCCAGCGAGATGCTCTCAACAGAGCTGATA 1077
 QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProIysProAspPhe 200
 DB 1078 CAGCAGATGGGATTTGTTATGTGTTAAATGCCAGCTAATACCTGTCCAAAGCTGACTTT 1137
 QY 201 IleProIleSerHisPheLeuArgValProValAsnAspSerPheCysGluIleLeu 220
 DB 1138 ATCCCGAGCTCATTTCCGCGTGGCTGCTGATGACAGCTTTGTGAGAAATTTTG 1197
 QY 221 ProTyrLeuAspIleSerValAspPheIleGluValAlaIleAsnArgIleCysVal 240
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 QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
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 QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluIleValArgProThr 280
 DB 1318 AAGAGATGAGACATGCTTAAATGAGAGCTTACAGATTGTGAAAGAAAGAAAGCACTACT 1377
 QY 281 IleSerProAsnPheAsnIleLeuGlnIleLeuAspTyrGluIleValIleValAsn 300
 DB 1378 AATATCCCAAACTCAATTTTCTGGGCCCAACTCTGACCTATGAGAGAAAGATTAAGAAC 1437
 QY 301 GlnThrGlyAlaSerGlyProIysSerIleValLeuLeuHisIleuGluIleValProAsn 320
 DB 1438 CAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGCTGCACTTGAGAAAGCCAAAT 1497
 QY 321 GluProValProAlaValSerGluGlyGlnIleValSerGluThrProLeuSerProPro 340
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 DB 1558 TGTGCCAGCTCTGCTACCTCAGAGGACAGCAAGAGCCCTGTGATCCCGCCACAGGTG 1617
 QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
 DB 1618 CCCAGGCTGCCAGCTGACGCCGTGCTGTTTAAAGACAGCCCGCTGTACAGGGGCTC 1677
 QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluIleAspSerAsnIleValIleValSerPhe 400
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 QY 401 SerLeuAspIleIleValSerValSerTyrSerAlaSerMetAlaIleSerLeuHisGlyPhe 420
 DB 1738 TCTCTGATATCAAAACATTTTCAATTTCAAGCCAGCATGAGCACTTACATGGCTTC 1797
 QY 421 SerSerSerGluAspAlaLeuGluIleTyrIleValProSerThrThrLeuAspGlyThrAsn 440
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QY 461 AspLysGluGlnAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1918 GATTAAGGAGGAAGCCAGCATCCCAAGAACTGACAGACGCCAGGCTTCAGACAGCCAG 1977
QY 491 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 1978 AGCAAGCGATTGCATTCGGTCAGAACCCAGACAGAGTGCCACGCCAGAGGCTCCCTTTTA 2037
QY 501 SerProLeuHisArgSerGlySerValGlnAspAsnTyrHisThrSerPheLeuPheGly 520
Db 2038 TCTCCACTGCATCGAAGTGGAAGCGCTGGAGGACAAATTACACACAGGCTTCCTTTTCGGC 2097
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
Db 2098 CTTTCCACCAAGCCAGACAGACACTCACGAAGTCTGCTGGGCTTGAAGGCTGGGAC 2157
QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db 2158 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACACAGCAGCTGGTATTTGCC 2217
QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580
Db 2218 ACAAGTCTCTACACTTCTACTCTGCTCAGCCACTTACGAGGAGGAGTGCAGTTACTCT 2277
QY 581 AlaTyrSerCySerSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
Db 2278 GCTTACAGCTGACAGCTGCTGCCACTTGGCGGAGACCAAGTCTATTTCTGTGCGCAGGCG 2337
QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGluGluSerProPheGlu 620
Db 2338 CAGAAAGCCAAAGTGAAGAAGCTGACTCGCGGCGAGCTGGCATGAAAGAGAGCCCTTGAA 2397
QY 621 LysGlnPheLysArgArgSerCySerGlnMetGluPheGlyGluSerIleMetSerGluAsn 640
Db 2398 AAGCAGTTTAAACCCAGAAAGCTGCCAATGGAATTTGAGAGAGCATCATGTCAAGAAC 2457
QY 641 ArgSerArgGluGlnLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db 2458 AGGTCAAGGAGAAAGCTGGGGAAGAGTGGCAGTCAGTCTAGCTTTTTCGGGACGATGGAA 2517
QY 661 IleIleGluValSer 665
Db 2518 ATCATTGAGGCTCTCC 2532
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Search completed: June 24, 2004, 00:04:41
Job time : 624 secs

GenCore version 5.1.6
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OM proteIn - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 23:00:42 ; Search time 3667 Seconds

(without alignments)
5415.421 Million cell updates/sec

Title: US-10-029-345A-109
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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Command line parameters:

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-Q/cqn2_1/USPTO.spool.p/US10029345/runat 23062004 121752 25604/app query.fasta_1.839
-DB=EST -QFMT=fastap -SUFPRX=ol12.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=75
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-OUTFMT=pro -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Database :

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7: em_estro: *
8: em_hic: *
9: gb_est1: *
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12: gb_est3: *
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23: em_gss_mus: *
24: em_gss_pro: *
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26: em_gss_phg: *
27: em_gss_vr1: *
28: gb_gss1: *

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found					

Search completed: June 24, 2004, 02:47:42
Job time : 3667 secs

GenCore version 5.1.6
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No matches found

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 23:54:21 ; Search time 666 Seconds
(without alignments)
4574.211 Million cell updates/sec

Search completed: June 24, 2004, 03:01:36
Job time : 666 secs

Title: US-10-029-345A-109

Perfect score: 665

Sequence: 1 MAHEMIGTGYTERLVALL.....LAKVGSQSFSGSMETIEVS 665

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Word size: 473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1p
-Q/cgn2_1/USPTO.spool.p/US10029345/runat.23062004.121753.25636/app.query.faeta_1.839
-DB=Published Applications NA -QFMT=faesad -SUFFIX=ol12.rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human0.cgi -LIST=75 -DOCCALIGN=200 -THR_SCORE=quality -THR_MIN=473
-ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10029345 @CGN 1 1 723 @runat.23062004.121753.25636
-NGPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGIOQ -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-Fgapop=6 -Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Query Length	DB ID	Description
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 23:25:13 ; Search time 139 Seconds
(without alignments)
2654.981 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 665
Sequence: 1 MAHEMIGTQIVTERLVALLIE.....LGRVGSQSSEFSGSMETIEVS 665

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 473

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q/cgn2_1/uspto.spool.p/us10029345/runat.23062004.121753.25617/app.query.fasta_1.839
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=ol12.rnt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=75 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=473 -ALIGN=50 -MODE=LOCAL
-OUTFMT=plco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10029345 @CGN 1 1 105 @runat.23062004.121753.25617 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PCTUS.COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description

No matches found				

Search completed: June 24, 2004, 02:50:16
Job time : 139 secs

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